

10/572796  
IAP20 Rec'd PCTO 21 MAR 2006

SEQUENCE LISTING

<110> Steinkuhler, Christian  
Lahm, Armin  
Pallaoro, Michele  
Nardella, Caterina

<120> SYNTHETIC HEPARANASE MOLECULES AND USES  
THEREOF

<130> ITR0060YP

<150> PCT/EP2004/010517  
<151> 2004-09-17

<150> 60/537,729  
<151> 2004-01-20

<150> 60/506,479  
<151> 2003-09-26

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<211> 15

<212> PRT

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<223> Peptide

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 Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu Arg Thr Leu  
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 Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr  
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Leu Gly Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile		
65	70	75
Asn Gly Ser Gln Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu		
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Arg Lys Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly		
100	105	110
Gln Pro Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala		
115	120	125
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130	135	140
Gly Arg Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp		
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Ile Phe Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr		
165	170	175
Arg Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly		
180	185	190
Gly Gly Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp		
195	200	205
Leu Asp Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met		
210	215	220
Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn		
225	230	235
Phe Asp Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu		
245	250	255
Val Gly Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg		
260	265	270
Lys Leu Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr		
275	280	285
Lys Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr		
290	295	300
Lys Tyr Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys		
305	310	315
		320

Tyr Leu Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val  
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 Pro Leu Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro  
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 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
                   50                                  55                                  60  
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
   65                                  70                                  75                                  80  
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
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 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Phe Lys Asn Ser  
                   100                                  105                                  110  
 Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys  
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Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala  
 130 135 140  
 Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys  
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 Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn  
 165 170 175  
 Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln Leu Gly  
 180 185 190  
 Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr Phe Lys  
 195 200 205  
 Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg Lys Thr  
 210 215 220  
 Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp  
 225 230 235 240  
 Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg  
 245 250 255  
 Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val  
 260 265 270  
 Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val  
 275 280 285  
 Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu  
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 Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu  
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 Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe Gly  
 325 330 335  
 Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu Pro Asp  
 340 345 350  
 Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys Val Leu  
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 Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val Tyr Leu  
 370 375 380  
 His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp Leu Thr  
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Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly Leu Thr
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          450              455              460
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<211> 1479

<212> DNA

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<223> hep 106

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Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Lys	Lys	Phe
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Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu
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Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu
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Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn

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 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
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 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
 85 90 95  
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Gly Ser Gly  
 100 105 110  
 Ser Gly Ser Lys Lys Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val  
 115 120 125  
 Asp Val Leu Tyr Thr Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe  
 130 135 140  
 Gly Leu Asn Ala Leu Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser  
 145 150 155 160  
 Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile  
 165 170 175

Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp		
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Ile Phe Ile Asn Gly Ser Gln Leu Gly Glu Asp Phe Ile Gln Leu His		
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Lys Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro		
210	215	220
Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe		
225	230	235
Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val Thr Trp His His Tyr		
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Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp		
260	265	270
Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val Phe Gln Val Val		
275	280	285
Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser		
290	295	300
Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly		
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Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu		
325	330	335
Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val		
340	345	350
Asp Glu Asn Phe Asp Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe		
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Lys Lys Leu Val Gly Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser		
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Lys Arg Arg Lys Leu Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn		
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Pro Arg Tyr Lys Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His		
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420	425	430
Val Asp Lys Tyr Leu Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser		
435	440	445
Lys Ser Val Gln Leu Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln		
450	455	460
Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu		

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<213> Artificial Sequence

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<210> 24

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> hep GS6

<400> 24

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<210> 25

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> hep GS-A4

<400> 25

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Leu	Leu	Gly	Pro	Leu	Gly	Pro	Leu	Ser	Pro	Gly	Ala	Leu	Pro	Arg	Pro
			20					25					30		
Ala	Gln	Ala	Gln	Asp	Val	Val	Asp	Leu	Asp	Phe	Phe	Thr	Gln	Glu	Pro
		35					40					45			
Leu	His	Leu	Val	Ser	Pro	Ser	Phe	Leu	Ser	Val	Thr	Ile	Asp	Ala	Asn
	50					55					60				
Leu	Ala	Thr	Asp	Pro	Arg	Phe	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	Leu
65					70					75				80	
Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	Gly
			85						90				95		
Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Ser	Thr	Phe
		100						105				110			
Glu	Glu	Arg	Ser	Tyr	Trp	Gly	Ser	Gly	Ala	Gly	Ser	Gly	Ala	Glu	Trp
		115				120					125				
Pro	Tyr	Gln	Glu	Gln	Leu	Leu	Leu	Arg	Glu	His	Tyr	Gln	Lys	Lys	Phe
	130					135					140				
Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe
145				150					155					160	
Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu
			165						170					175	
Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu

	180		185		190										
Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn
	195						200					205			
Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser
	210						215					220			
Gln	Leu	Gly	Glu	Asp	Phe	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser
225						230				235					240
Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg
				245					250					255	
Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu
			260					265					270		
Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr
	275						280					285			
Ala	Thr	Arg	Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile
	290						295				300				
Ser	Ser	Val	Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly
305					310					315				320	
Lys	Lys	Val	Trp	Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Gly	Ala
				325					330				335		
Pro	Leu	Leu	Ser	Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys
			340					345					350		
Leu	Gly	Leu	Ser	Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val
	355						360					365			
Phe	Phe	Gly	Ala	Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro
	370					375					380				
Leu	Pro	Asp	Tyr	Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr
385					390					395				400	
Lys	Val	Leu	Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg
			405					410					415		
Val	Tyr	Leu	His	Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly
	420						425					430			
Asp	Leu	Thr	Leu	Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu
	435						440					445			
Arg	Leu	Pro	Tyr	Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu
	450					455					460				
Arg	Pro	Leu	Gly	Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn
465					470					475				480	

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
                           485                          490                          495  
 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser  
                           500                          505                          510  
 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
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<210> 26

<211> 507

<212> PRT

<213> Artificial Sequence

<220>

<223> hep GS-A6

<400> 26

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 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro  
                           20                          25                          30  
 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
                           35                          40                          45  
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
                           50                          55                          60  
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
   65                          70                          75                          80  
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
                           85                          90                          95  
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Gly Ser Gly  
                           100                          105                          110  
 Ser Gly Ser Gly Ser Gly Ser Gly Ser Lys Lys Phe Lys Asn Ser Thr  
                           115                          120                          125  
 Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys Ser  
                           130                          135                          140  
 Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala Asp  
   145                          150                          155                          160

Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu	Asp	Tyr	Cys	Ser			
																165	170	175
Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn	Glu	Pro	Asn	Ser			
																180	185	190
Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser	Gln	Leu	Gly	Glu			
																195	200	205
Asp	Phe	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser	Thr	Phe	Lys	Asn			
																210	215	220
Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg	Arg	Lys	Thr	Ala			
																225	230	235
Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu	Val	Ile	Asp	Ser			
																245	250	255
Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr	Ala	Thr	Arg	Glu			
																260	265	270
Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile	Ser	Ser	Val	Gln			
																275	280	285
Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly	Lys	Lys	Val	Trp			
																290	295	300
Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Gly	Ala	Pro	Leu	Leu	Ser			
																305	310	315
Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys	Leu	Gly	Leu	Ser			
																325	330	335
Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val	Phe	Phe	Gly	Ala			
																340	345	350
Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro	Leu	Pro	Asp	Tyr			
																355	360	365
Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr	Lys	Val	Leu	Met			
																370	375	380
Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg	Val	Tyr	Leu	His			
																385	390	395
Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly	Asp	Leu	Thr	Leu			
																405	410	415
Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu	Arg	Leu	Pro	Tyr			
																420	425	430
Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu	Arg	Pro	Leu	Gly			
																435	440	445
Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn	Gly	Leu	Thr	Leu			

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      450              455              460
Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu Lys Pro Leu
465              470              475              480
Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe
      485              490              495
Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
      500              505

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<210> 27

<211> 526

<212> PRT

<213> Artificial Sequence

<220>

<223> hep Hya1

<400> 27

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Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
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      20              25              30
Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
      35              40              45
Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
      50              55              60
Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65              70              75              80
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
      85              90              95
Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
      100              105              110
Glu Glu Arg Ser Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Trp Pro
      115              120              125
Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys
      130              135              140
Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala

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145	150	155	160
Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg			
	165	170	175
Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp			
	180	185	190
Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu			
	195	200	205
Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln			
	210	215	220
Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr			
225	230	235	240
Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg			
	245	250	255
Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val			
	260	265	270
Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala			
	275	280	285
Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser			
	290	295	300
Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys			
305	310	315	320
Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro			
	325	330	335
Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu			
	340	345	350
Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe			
	355	360	365
Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu			
	370	375	380
Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys			
385	390	395	400
Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val			
	405	410	415
Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp			
	420	425	430
Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu Arg			
	435	440	445



Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu Arg  
 450 455 460  
 Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly  
 465 470 475 480  
 Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu  
 485 490 495  
 Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr  
 500 505 510  
 Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
 515 520 525

<210> 28

<211> 1581

<212> DNA

<213> Artificial Sequence

<220>

<223> hep Hya1

<400> 28

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 ctggacttct tcacccagga gccgctgcac ctgggtgagcc cctcgttctt gtccgtcacc 180  
 attgacgcca acctggccac ggacccgcgg ttcctcatcc tcctgggttc tccaaagctt 240  
 cgtaccttgg ccagaggctt gtctcctgcg tacctgaggt ttggtggcac caagacagac 300  
 ttcctaattt tcgatcccaa gaaggaatca acctttgaag agagaagtta ctgggccttc 360  
 aaggacaaga cccccgaatg gccctaccag gagcaattgc tactccgaga aactaccag 420  
 aaaaagttca agaacagcac ctactcaaga agctctgtag atgtgctata cacttttgca 480  
 aactgctcag gactggactt gatctttggc cttaaagcgt tattaagaac agcagatttg 540  
 cagtggaaca gttctaattg tcagttgctc ctggactact gctcttccaa ggggtataac 600  
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 aatgggtcgc agttaggaga agattttatt caattgcata aacttctaag aaagtccacc 720  
 ttcaaaaatg caaaactcta tggctctgat gttggctcag ctcgaagaaa gacggctaag 780  
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gaagtgggtga tgaggcaagt attcttttga gcaggaaact accatttagt ggatgaaaac 1140
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ccaggaagtt cactgggctt gccagctttc tcatatagtt tttttgtgat aagaaatgcc 1560
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<210> 29

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> hep TEV110-158

<400> 29

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Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
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      20             25             30
Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
      35             40             45
Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
      50             55             60
Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
      65             70             75             80
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
      85             90             95
Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Gly Ser Gly
      100            105            110
Ser Glu Asn Leu Tyr Phe Gln Gly Ser Gly Ser Thr Phe Glu Glu Arg
      115            120            125

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Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly Ser
  130                      135                      140
Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr Gln
145                      150                      155                      160
Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Ser Gly Ser Gly Glu Asn
                      165                      170                      175
Leu Tyr Phe Gln Gly Ser Gly Ser Lys Lys Phe Lys Asn Ser Thr Tyr
                      180                      185                      190
Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys Ser Gly
                      195                      200                      205
Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala Asp Leu
  210                      215                      220
Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser
225                      230                      235                      240
Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe
                      245                      250                      255
Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln Leu Gly Glu Asp
                      260                      265                      270
Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala
                      275                      280                      285
Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys
  290                      295                      300
Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val
305                      310                      315                      320
Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp
                      325                      330                      335
Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys
                      340                      345                      350
Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu
                      355                      360                      365
Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asp
  370                      375                      380
Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala
385                      390                      395                      400
Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly
                      405                      410                      415
Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu Pro Asp Tyr Trp

```

420	425	430
Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys Val Leu Met Ala		
435	440	445
Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val Tyr Leu His Cys		
450	455	460
Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp Leu Thr Leu Tyr		
465	470	475
Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu Arg Leu Pro Tyr Pro		
485	490	495
Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu Arg Pro Leu Gly Pro		
500	505	510
His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly Leu Thr Leu Lys		
515	520	525
Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg		
530	535	540
Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe Val		
545	550	555
Ile Arg Asn Ala Lys Val Ala Ala Cys Ile		
565	570	

&lt;210&gt; 30

&lt;211&gt; 1668

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hep TEV110

&lt;400&gt; 30

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ctggacttct tcaccagga gccgctgcac ctggtgagcc cctcgttcct gtccgtcacc 180
attgacgcca acctggccac ggacccgcgg ttcctcatcc tcttgggttc tccaaagctt 240
cgtaccttgg ccagaggctt gtctcctgcg tacctgaggt ttggtggcac caagacagac 300
ttcctaattt tcgatcccaa gaaggaaggc agcggatctg agaacctgta cttccagggt 360
tccggttcaa cttttgaaga gagaagttac tggcaatctc aagtcaacca ggatatttgc 420

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aaatatggat ccatccctcc tgatgtggag gagaagttac ggttggaatg gccctaccag 480
gagcaattgc tactccgaga acactaccag aaaaagttca agaacagcac ctactcaaga 540
agctctgtag atgtgctata cacttttgca aactgctcag gactggactt gatctttggc 600
ctaaatgcgt tattaagaac agcagatttg cagtggaaca gttctaatagc tcagttgctc 660
ctggactact gctcttccaa ggggtataac atttcttggg aactaggcaa tgaacctaac 720
agtttcctta agaaggctga tattttcatc aatgggtcgc agttaggaga agattttatt 780
caattgcata aacttctaag aaagtccacc ttcaaaaatg caaaactcta tggctctgat 840
gttggtcagc ctcaagaaa gacggctaag atgctgaaga gcttcctgaa ggctggtgga 900
gaagtgattg attcagttac atggcatcac tactatttga atggacggac tgctaccagg 960
gaagattttc taaaccctga tgtattggac atttttattt catctgtgca aaaagttttc 1020
caggtgggtg agagcaccag gcctggcaag aaggtctggt taggagaaac aagctctgca 1080
tatggaggcg gagcgccctt gctatccgac acctttgcag ctggctttat gtggctggat 1140
aaattgggcc tgtcagcccg aatgggaata gaagtgggtga tgaggcaagt attctttgga 1200
gcaggaaact accatttagt ggatgaaaac ttcgatcctt tacctgatta ttggctatct 1260
cttctgttca agaaattggt gggcaccaag gtgttaatgg caagcgtgca aggttcaaag 1320
agaaggaagc ttcgagtata ccttcattgc acaaactg acaatccaag gtataaagaa 1380
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tattcttttt ctaacaagca agtggataaa taccttctaa gacctttggg acctcatgga 1500
ttactttcca aatctgtcca actcaatggt ctaactctaa agatgggtgga tgatcaaacc 1560
ttgccacctt taatggaaaa acctctccgg ccaggaagtt cactgggctt gccagctttc 1620
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<210> 31

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> hep TEV110

<400> 31

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Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
 1             5             10             15
Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
          20             25             30
Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
          35             40             45

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Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
  50                      55                      60
Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65                      70                      75                      80
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
                      85                      90                      95
Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Gly Ser Gly
                      100                      105                      110
Ser Glu Asn Leu Tyr Phe Gln Gly Ser Gly Ser Thr Phe Glu Glu Arg
                      115                      120                      125
Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly Ser
                      130                      135                      140
Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr Gln
                      145                      150                      155                      160
Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys Asn Ser
                      165                      170                      175
Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys
                      180                      185                      190
Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala
                      195                      200                      205
Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys
                      210                      215                      220
Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn
                      225                      230                      235                      240
Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln Leu Gly
                      245                      250                      255
Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr Phe Lys
                      260                      265                      270
Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg Lys Thr
                      275                      280                      285
Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp
                      290                      295                      300
Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg
                      305                      310                      315                      320
Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val
                      325                      330                      335
Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val

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          340          345          350
Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu
          355          360          365
Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu
          370          375          380
Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe Gly
385          390          395          400
Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu Pro Asp
          405          410          415
Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys Val Leu
          420          425          430
Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val Tyr Leu
          435          440          445
His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp Leu Thr
          450          455          460
Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu Arg Leu Pro
465          470          475          480
Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu Arg Pro Leu
          485          490          495
Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly Leu Thr
          500          505          510
Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu Lys Pro
          515          520          525
Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe
          530          535          540
Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
545          550          555

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<210> 32

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> hep TEV110/158

<400> 32

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ctgggtcccc tctcccttgg cgccctgccc cgacctgcgc aagcacagga cgtcgtggac 120
ctggactttct tcaccagga gccgctgcac ctggtgagcc cctcgttcct gtccgtcacc 180
attgacgcca acctggccac ggacccgcgg ttcctcatcc tctgggttc tccaaagctt 240
cgtaccttgg ccagaggctt gtctcctgcg tacctgaggt ttggtggcac caagacagac 300
ttcctaattt tcgatcccaa gaaggaaggc agcggatctg agaacctgta cttccagggt 360
tccggttcaa cctttgaaga gagaagttac tggcaatctc aagtcaacca ggatatttgc 420
aaatatggat ccatccctcc tgatgtggag gagaagttac gggtggaatg gccctaccag 480
gagcaattgc tactccgaga aactaccag tctggatccg gtgaaaatct ctattttcag 540
ggctcaggaa gtaaaaagtt caagaacagc acctactcaa gaagctctgt agatgtgcta 600
tacacttttg caaactgctc aggactggac ttgatctttg gcctaaatgc gttattaaga 660
acagcagatt tgcagtggaa cagttctaata gctcagttgc tctggacta ctgctcttcc 720
aaggggtata acatttcttg ggaactaggc aatgaaccta acagtttctt taagaaggct 780
gatattttca tcaatgggtc gcagtttaga gaagatttta ttcaattgca taaacttcta 840
agaaagtcca ccttcaaaaa tgcaaaactc tatggtcctg atgttggtca gcctcgaaga 900
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aggcctggca agaaggctct gttaggagaa acaagctctg catatggagg cggagcgccc 1140
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cgaatgggaa tagaagtggg gatgaggcaa gtattctttg gagcaggaaa ctaccattta 1260
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gtgggcacca aggtgttaat ggcaagcgtg caaggttcaa agagaaggaa gcttcgagta 1380
taccttcatt gcacaaacac tgacaatcca aggtataaag aaggagattt aactctgtat 1440
gccataaacc tcataatgt caccaagtac ttgcggttac cctatccttt ttctaacaag 1500
caagtggata aataccttct aagacctttg ggacctcatg gattactttc caaatctgtc 1560
caactcaatg gtctaactct aaagatggtg gatgatcaaa ccttgccacc tttaatggaa 1620
aaacctctcc ggccaggaag ttcactgggc ttgccagctt tctcatatag tttttttgtg 1680
ataagaaatg ccaaagttgc tgcttgcac 1710

```

<210> 33

<211> 174

<212> PRT

<213> Homo Sapiens

<400> 33



Gln Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro Leu His  
 1 5 10 15  
 Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn Leu Ala  
 20 25 30  
 Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu Arg Thr  
 35 40 45  
 Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys  
 50 55 60  
 Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe Glu Glu  
 65 70 75 80  
 Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly  
 85 90 95  
 Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr  
 100 105 110  
 Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys Asn  
 115 120 125  
 Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn  
 130 135 140  
 Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr  
 145 150 155 160  
 Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
 165 170

<210> 34  
 <211> 174  
 <212> PRT  
 <213> Mus Musculus

<400> 34  
 Thr Asp Asp Val Val Asp Leu Glu Phe Tyr Thr Lys Arg Pro Leu Arg  
 1 5 10 15  
 Ser Val Ser Pro Ser Phe Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala  
 20 25 30  
 Thr Asp Pro Arg Phe Leu Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala  
 35 40 45  
 Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys

```

      50              55              60
Thr Asp Phe Leu Ile Phe Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu
65              70              75              80
Arg Ser Tyr Trp Lys Ser Gln Val Asn His Asp Ile Cys Arg Ser Glu
      85              90              95
Pro Val Ser Ala Ala Val Leu Arg Lys Leu Gln Val Glu Trp Pro Phe
      100             105             110
Gln Glu Leu Leu Leu Leu Arg Glu Gln Tyr Gln Lys Glu Phe Lys Asn
      115             120             125
Ser Thr Tyr Ser Arg Ser Ser Val Asp Met Leu Tyr Ser Phe Ala Lys
      130             135             140
Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr
      145             150             155             160
Pro Asp Leu Arg Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
      165             170

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```

<210> 35
<211> 174
<212> PRT
<213> Bos taurus

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```

<400> 35
Ala Asp Asp Ala Ala Glu Leu Glu Phe Phe Thr Glu Arg Pro Leu His
 1              5              10              15
Leu Val Ser Pro Ala Phe Leu Ser Phe Thr Ile Asp Ala Asn Leu Ala
      20              25              30
Thr Asp Pro Arg Phe Phe Thr Phe Leu Gly Ser Ser Lys Leu Arg Thr
      35              40              45
Leu Ala Arg Gly Leu Ala Pro Ala Tyr Leu Arg Phe Gly Gly Asn Lys
      50              55              60
Gly Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Pro Ala Phe Glu Glu
65              70              75              80
Arg Ser Tyr Trp Leu Ser Gln Ser Asn Gln Asp Ile Cys Lys Ser Gly
      85              90              95
Ser Ile Pro Ser Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Phe
      100             105             110

```

Gln Glu Gln Val Leu Leu Arg Glu Gln Tyr Gln Lys Lys Phe Thr Asn  
 115 120 125  
 Ser Thr Tyr Ser Arg Ser Ser Val Asp Met Leu Tyr Thr Phe Ala Ser  
 130 135 140  
 Cys Ser Gly Leu Asn Leu Ile Phe Gly Val Asn Ala Leu Leu Arg Thr  
 145 150 155 160  
 Thr Asp Met His Trp Asp Ser Ser Asn Ala Gln Leu Leu Leu  
 165 170

<210> 36  
 <211> 173  
 <212> PRT  
 <213> Gallus Gallus

<400> 36  
 Pro Arg Arg Thr Ala Glu Leu Gln Leu Gly Leu Arg Glu Pro Ile Gly  
 1 5 10 15  
 Ala Val Ser Pro Ala Phe Leu Ser Leu Thr Leu Asp Ala Ser Leu Ala  
 20 25 30  
 Arg Asp Pro Arg Phe Val Ala Leu Leu Arg His Pro Lys Leu His Thr  
 35 40 45  
 Leu Ala Ser Gly Leu Ser Pro Gly Phe Leu Arg Phe Gly Gly Thr Ser  
 50 55 60  
 Thr Asp Phe Leu Ile Phe Asn Pro Asn Lys Asp Ser Thr Trp Glu Glu  
 65 70 75 80  
 Lys Val Leu Ser Glu Phe Gln Ala Lys Asp Val Cys Glu Ala Trp Pro  
 85 90 95  
 Ser Phe Ala Val Val Pro Lys Leu Leu Leu Thr Gln Trp Pro Leu Gln  
 100 105 110  
 Glu Lys Leu Leu Leu Ala Glu His Ser Trp Lys Lys His Lys Asn Thr  
 115 120 125  
 Thr Ile Thr Arg Ser Thr Leu Asp Ile Leu His Thr Phe Ala Ser Ser  
 130 135 140  
 Ser Gly Phe Arg Leu Val Phe Gly Leu Asn Ala Leu Leu Arg Arg Ala  
 145 150 155 160  
 Gly Leu Gln Trp Asp Ser Ser Asn Ala Lys Gln Leu Leu

165

170

&lt;210&gt; 37

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 37

Glu Lys Thr Leu Ile Leu Leu Asp Val Ser Thr Lys Asn Pro Val Arg  
 1 5 10 15

Thr Val Asn Glu Asn Phe Leu Ser Leu Gln Leu Asp Pro Ser Ile Ile  
 20 25 30

His Asp Gly Trp Leu Asp Phe Leu Ser Ser Lys Arg Leu Val Thr Leu  
 35 40 45

Ala Arg Gly Leu Ser Pro Ala Phe Leu Arg Phe Gly Gly Lys Arg Thr  
 50 55 60

Asp Phe Leu Gln Phe Gln Asn Leu Arg Asn Pro Ala Lys Ser Arg Gly  
 65 70 75 80

Gly Pro Gly Pro Asp Tyr Tyr Leu Lys Asn Tyr Glu Asp Asp Ile Val  
 85 90 95

Arg Ser Asp Val Ala Leu Asp Lys Gln Lys Gly Cys Lys Ile Ala Gln  
 100 105 110

His Pro Asp Val Met Leu Glu Leu Gln Arg Glu Lys Ala Ala Gln Met  
 115 120 125

His Leu Val Leu Leu Lys Glu Gln Phe Ser Asn Thr Tyr Ser Asn Leu  
 130 135 140

Ile Leu Thr Ala Arg Ser Leu Asp Lys Leu Tyr Asn Ser Ala Asp Cys  
 145 150 155 160

Ser Gly Leu His Leu Ile Phe Ala Leu Asn Ala Leu Arg Arg Asn Pro  
 165 170 175

Asn Asn Ser Trp Asn Ser Ser Ser Ala Leu Ser Leu Leu  
 180 185

&lt;210&gt; 38

&lt;211&gt; 151

<212> PRT

<213> Bombyx Mori

<400> 38

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Val Arg Tyr Phe Val Thr Ile Asn Glu Asn Gln Glu Asp Ile Lys Leu
 1             5             10             15
Ile Ser Glu Asp Phe Leu Ser Phe Gly Ile Asp Thr Ile Glu Ile Glu
      20             25             30
Asn Tyr Asn Arg Ile Asn Tyr Ser Asp Thr Arg Leu Arg Glu Leu Ala
      35             40             45
Ala Ala Leu Ser Pro Ala Arg Leu Arg Leu Gly Gly Thr Met Ser Glu
      50             55             60
Arg Leu Ile Phe Ser Lys Glu Asn Ile Pro Ile Ser Cys His Asn Cys
65             70             75             80
Ser Tyr Lys Ser Tyr Pro Lys Ser Leu Cys Gln Leu Ile Glu Lys Pro
      85             90             95
Cys Lys His Lys His Lys Phe Leu Pro Phe Phe Ile Met Thr Gly Asn
      100            105            110
Glu Trp Asn Gln Ile Asn Asp Phe Cys Arg Lys Thr Asn Leu Lys Leu
      115            120            125
Leu Phe Ser Leu Asn Ala Met Leu Arg Asp Asn His Gly Trp Asn Glu
      130            135            140
Lys Asn Ala Arg Glu Leu Ile
145            150

```

<210> 39

<211> 147

<212> PRT

<213> Hirudinaria manillensis

<400> 39

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Lys Asn Val Ile Ala Ser Val Ser Glu Ser Phe His Gly Val Ala Phe
 1             5             10             15
Asp Ala Ser Leu Phe Ser Pro Lys Gly Pro Trp Ser Phe Val Asn Ile
      20             25             30
Thr Ser Pro Lys Leu Phe Lys Leu Leu Glu Gly Leu Ser Pro Gly Tyr

```

35	40	45
Phe Arg Val Gly Gly Thr	Phe Ala Asn Trp Leu	Phe Phe Asp Leu Asp
50	55	60
Glu Asn Asn Lys Trp Lys Asp Tyr Trp Ala Phe Lys Asp Lys Thr Pro		
65	70	75
Glu Thr Ala Thr Ile Thr Arg Arg Trp Leu Phe Arg Lys Gln Asn Asn		
85	90	95
Leu Lys Lys Glu Thr Phe Asp Asp Leu Val Lys Leu Thr Lys Gly Ser		
100	105	110
Lys Met Arg Leu Leu Phe Asp Leu Asn Ala Glu Val Arg Thr Gly Tyr		
115	120	125
Glu Ile Gly Lys Lys Thr Thr Ser Thr Trp Asp Ser Ser Glu Ala Glu		
130	135	140
Lys Leu Phe		
145		

<210> 40

<211> 150

<212> PRT

<213> *Scutellaria baicallensis*

<400> 40

Asn Tyr Val Cys Ala Thr Leu Asp Leu Trp Pro Pro Thr Lys Cys Asn
1 5 10 15
Tyr Gly Asn Cys Pro Trp Gly Lys Ser Ser Phe Leu Asn Leu Asp Leu
20 25 30
Asn Asn Asn Ile Ile Arg Asn Ala Val Lys Glu Phe Ala Pro Leu Lys
35 40 45
Leu Arg Phe Gly Gly Thr Leu Gln Asp Arg Leu Val Tyr Gln Thr Ser
50 55 60
Arg Asp Glu Pro Cys Asp Ser Thr Phe Tyr Asn Asn Thr Asn Leu Ile
65 70 75 80
Leu Asp Phe Ser His Ala Cys Leu Ser Leu Asp Arg Trp Asp Glu Ile
85 90 95
Asn Gln Phe Ile Leu Glu Thr Gly Ser Glu Ala Val Phe Gly Leu Asn
100 105 110

Ala Leu Arg Gly Lys Thr Val Glu Ile Lys Gly Ile Ile Lys Asp Gly  
 115 120 125  
 Gln Tyr Leu Gly Glu Thr Thr Thr Ala Val Gly Glu Trp Asp Tyr Ser  
 130 135 140  
 Asn Ser Lys Phe Leu Ile  
 145 150

<210> 41  
 <211> 138  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 41  
 Asn Phe Val Cys Ala Thr Leu Asp Trp Trp Pro His Asp Lys Cys Asn  
 1 5 10 15  
 Tyr Asp Gln Cys Pro Trp Gly Tyr Ser Ser Val Ile Asn Met Asp Leu  
 20 25 30  
 Thr Arg Pro Leu Leu Thr Lys Ala Ile Lys Ala Phe Lys Pro Leu Arg  
 35 40 45  
 Ile Arg Ile Gly Gly Ser Leu Gln Asp Gln Val Ile Tyr Asp Val Gly  
 50 55 60  
 Asn Leu Lys Thr Pro Cys Arg Pro Phe Gln Lys Met Asn Ser Gly Leu  
 65 70 75 80  
 Phe Gly Phe Ser Lys Gly Cys Leu His Met Lys Arg Trp Asp Glu Leu  
 85 90 95  
 Asn Ser Phe Leu Thr Ala Thr Gly Ala Val Val Thr Phe Gly Leu Asn  
 100 105 110  
 Ala Leu Arg Gly Arg His Lys Leu Arg Gly Lys Ala Trp Gly Gly Ala  
 115 120 125  
 Trp Asp His Ile Asn Thr Gln Asp Phe Leu  
 130 135

<210> 42  
 <211> 138  
 <212> PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 42

Asp Phe Ile Cys Ala Thr Leu Asp Trp Trp Pro Pro Glu Lys Cys Asp  
 1 5 10 15  
 Tyr Gly Ser Cys Ser Trp Asp His Ala Ser Ile Leu Asn Leu Asp Leu  
 20 25 30  
 Asn Asn Val Ile Leu Gln Asn Ala Ile Lys Ala Phe Ala Pro Leu Lys  
 35 40 45  
 Ile Arg Ile Gly Gly Thr Leu Gln Asp Ile Val Ile Tyr Glu Thr Pro  
 50 55 60  
 Asp Ser Lys Gln Pro Cys Leu Pro Phe Thr Lys Asn Ser Ser Ile Leu  
 65 70 75 80  
 Phe Gly Tyr Thr Gln Gly Cys Leu Pro Met Arg Arg Trp Asp Glu Leu  
 85 90 95  
 Asn Ala Phe Phe Arg Lys Thr Gly Thr Lys Val Ile Phe Gly Leu Asn  
 100 105 110  
 Ala Leu Ser Gly Arg Ser Ile Lys Ser Asn Gly Glu Ala Ile Gly Ala  
 115 120 125  
 Trp Asn Tyr Thr Asn Ala Glu Ser Phe Ile  
 130 135

&lt;210&gt; 43

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 43

Asn Phe Ile Cys Ala Thr Leu Asp Trp Trp Pro Pro Glu Lys Cys Asn  
 1 5 10 15  
 Tyr Asp Gln Cys Pro Trp Gly Tyr Ala Ser Leu Ile Asn Leu Asn Leu  
 20 25 30  
 Ala Ser Pro Leu Leu Ala Lys Ala Ile Gln Ala Phe Arg Thr Leu Arg  
 35 40 45  
 Ile Arg Ile Gly Gly Ser Leu Gln Asp Gln Val Ile Tyr Asp Val Gly  
 50 55 60



Asp	Leu	Lys	Thr	Pro	Cys	Thr	Gln	Phe	Lys	Lys	Thr	Asp	Asp	Gly	Leu
65					70				75					80	
Phe	Gly	Phe	Ser	Glu	Gly	Cys	Leu	Tyr	Met	Lys	Arg	Trp	Asp	Glu	Val
			85						90					95	
Asn	His	Phe	Phe	Asn	Ala	Thr	Gly	Ala	Ile	Val	Thr	Phe	Gly	Leu	Asn
			100					105					110		
Ala	Leu	His	Gly	Arg	Asn	Lys	Leu	Asn	Gly	Thr	Ala	Trp	Gly	Gly	Asp
		115					120					125			
Trp	Asp	His	Thr	Asn	Thr	Gln	Asp	Phe	Met						
	130					135									

<210> 44

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide

<400> 44

Ala	Phe	Lys	Asp	Lys	Thr	Pro
1				5		